

Supplementary Data

Beta diversity analysis

	Bray Curtis	Unweighted Unifrac	Weighted Unifrac
LZ_Diff-p	0.01	0.008	0.021
M_POULT_Diff-p	0.011	0.004	0.005
M_MEAT_Diff-p	0.026	0.034	0.049
V_ORANGE_Diff-p	0.026	0.186	0.033
LYCO_abs-b	0.027	0.118	0.059
M221_Diff-p	0.028	0.212	0.091
ALC_Diff-p	0.032	0.052	0.159
M161_abs-b	0.035	0.716	0.003
VITD_SUPP_abs-b	0.041	0.009	0.279
CAFF_SUPP_abs-b	0.049	0.251	0.052
CHOLN_SUPP_Diff-p	0.064	0.049	0.351
M_EGG_abs-b	0.073	0.005	0.26
V_POTATO_Diff-p	0.081	0.011	0.139
VB12_abs-b	0.084	0.026	0.042
CHOLE_abs-b	0.131	0.005	0.281
P205_abs-b	0.157	0.647	0.035
M_FISH_LO_Diff-p	0.261	0.026	0.243
D_MILK_Diff-p	0.353	0.379	0.023

LZ - Lutein and Zeaxanthin; M_POULT - Poultry; M_MEAT - Red Meat; V_ORANGE - Orange Vegetables; LYCO - Lycopene; M221 - Paullinic Acid; ALC - Alcohol (ethanol); M161 - Palmitoleic Acid; VITD - Vitamin D; CAFF - Caffeine; CHOLN - Choline; M_EGG - Eggs; V_POTATO - Potatoes; VB12 - Vitamin B12; CHOLE - Cholesterol; P205 - Eicosapentaenoic Acid; M_FISH_LO - Low Omega-3 Fish; D_MILK - Milk.

_abs-b: dichotomized by value at baseline time point

_Diff-p: dichotomized by percent change from baseline

SUPP[any of the above]: As above, but using the nutrient data including supplements.

Below are results from PERMANOVA comparing dichotomized groups of the above dietary variables. Variables that did not have OTUs with FDR $p < 0.10$ were not included. OTUs with FDR $p < 0.05$ are highlighted in yellow. Columns labeled 1_median and 2_median represent the OTU abundance medians for the low and high groups, respectively. Columns labeled 1_mean and 2_mean represent the OTU abundance means (proportions) for the low and high groups, respectively. Note that less abundant OTU means may sum to less than 0.000005 due to the original OTU table being generated and filtered from all samples at both time points.

PERMANOVA

ALC_Diff-p-h		Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L	OTU								
L3	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria	9.511998	0.002041	0.059199	0.059199	0.001726	0.000000	0.002418	0.000109
L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Lachnospiraceae;g__Shuttleworthia	12.382879	0.000433	0.079725	0.079725	0.000079	0.000000	0.000148	0.000000

CHOLE_abs-B-h		Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L	OTU								
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales	9.578272	0.001969	0.040191	0.096478	0.000309	0.000000	0.000490	0.000058
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales	9.415884	0.002151	0.040191	0.105406	0.000163	0.000000	0.000718	0.000028
L4	k__Bacteria;p__Firmicutes;Other;Other	9.159242	0.002475	0.040191	0.121258	0.000316	0.000000	0.001073	0.000087
L4	k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales	8.644261	0.003281	0.040191	0.160766	0.000237	0.000000	0.000419	0.000014
L2	k__Bacteria;p__[Thermi]	8.557956	0.003440	0.048162	0.048162	0.000401	0.000079	0.001098	0.000138
L6	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;Other	13.298507	0.000266	0.048874	0.048874	0.000081	0.000000	0.000927	0.000000
L3	k__Bacteria;p__Firmicutes;Other	9.159242	0.002475	0.049882	0.071765	0.000316	0.000000	0.001073	0.000087
L3	k__Bacteria;p__[Thermi];c__Deinococci	8.557956	0.003440	0.049882	0.099764	0.000401	0.000079	0.001098	0.000138
L5	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae	9.803256	0.001742	0.069188	0.177687	0.000080	0.000000	0.000194	0.000007
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae	9.415884	0.002151	0.069188	0.219416	0.000163	0.000000	0.000718	0.000028
L5	k__Bacteria;p__Firmicutes;Other;Other;Other	9.159242	0.002475	0.069188	0.252414	0.000316	0.000000	0.001073	0.000087
L5	k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae	8.644261	0.003281	0.069188	0.334655	0.000237	0.000000	0.000419	0.000014
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;Other	8.468114	0.003614	0.069188	0.368654	0.000161	0.000000	0.000210	0.000015
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae	8.252375	0.004070	0.069188	0.415127	0.000941	0.000078	0.003787	0.000415
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae]	7.622365	0.005765	0.084003	0.588018	0.000078	0.000000	0.000939	0.000000
L5	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae	7.289453	0.006936	0.088435	0.707478	0.000627	0.000079	0.001570	0.000210
L3	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria	6.727632	0.009493	0.091766	0.275299	0.003091	0.000535	0.013294	0.001234
L4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales	6.742862	0.009412	0.092241	0.461205	0.001881	0.000236	0.005526	0.002119
L2	k__Bacteria;p__Cyanobacteria	5.860207	0.015487	0.094764	0.216818	0.000173	0.000000	0.009548	0.000029
L2	k__Bacteria;p__Tenericutes	5.385346	0.020307	0.094764	0.284292	0.000242	0.000000	0.000952	0.000044

CHOLN_SUPP_Diff-p-h		Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L	OTU								
L2	k__Bacteria;p__Deferribacteres	7.622365	0.005765	0.080708	0.080708	0.000079	0.000000	0.000558	0.000000

LYCO_abs-B-h		Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L	OTU								
L5	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__	11.234043	0.000803	0.081917	0.081917	0.000000	0.000081	0.000000	0.000220

LZ_Diff-p-h		Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L	OTU								
L2	k__Bacteria;p__Verrucomicrobia	9.323392	0.002262	0.031675	0.031675	0.005567	0.000312	0.018291	0.001454
L5	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__	10.996407	0.000913	0.093114	0.093114	0.007557	0.000418	0.013543	0.003389
L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__g__	10.996407	0.000913	0.088582	0.167971	0.007557	0.000418	0.013543	0.003389
L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Peptococcaceae;g__rc4-4	10.473840	0.001211	0.088582	0.222781	0.000549	0.000000	0.001295	0.000569
L6	k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales;f__Erysipelotrichaceae;g__Allobaculum	10.148382	0.001444	0.088582	0.265747	0.008016	0.000314	0.025242	0.003092

M_EGG_abs-B-h		Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L	OTU								
L4	k__Bacteria;p__Firmicutes;Other;Other	11.795661	0.000594	0.011102	0.029091	0.000316	0.000000	0.001087	0.000073
L4	k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales	11.602388	0.000659	0.011102	0.032275	0.000237	0.000000	0.000426	0.000007
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales	11.543946	0.000680	0.011102	0.033305	0.000309	0.000000	0.000497	0.000051
L3	k__Bacteria;p__Firmicutes;Other	11.795661	0.000594	0.013237	0.017217	0.000316	0.000000	0.001087	0.000073
L3	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria	10.996407	0.000913	0.013237	0.026474	0.003091	0.000315	0.013415	0.001113
L3	k__Bacteria;p__[Thermi];c__Deinococci	9.344498	0.002237	0.021620	0.064860	0.000401	0.000079	0.001105	0.000131

L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales	9.415884	0.002151	0.022888	0.105406	0.000163	0.000000	0.000718	0.000028
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales	9.028659	0.002658	0.022888	0.130232	0.001082	0.000079	0.004152	0.000364
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales	8.931741	0.002803	0.022888	0.137326	0.001700	0.000262	0.005343	0.000604
L4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales	8.557956	0.003440	0.023566	0.168568	0.001881	0.000157	0.005562	0.002084
L4	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales	8.354441	0.003847	0.023566	0.188525	0.000801	0.000000	0.001120	0.000081
L3	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria	8.354441	0.003847	0.027894	0.111576	0.000801	0.000000	0.001120	0.000081
L2	k__Bacteria;p__[Thermi]	9.344498	0.002237	0.031312	0.031312	0.000401	0.000079	0.001105	0.000131
L5	k__Bacteria;p__Firmicutes;Other;Other;Other	11.795661	0.000594	0.033592	0.060556	0.000316	0.000000	0.001087	0.000073
L5	k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae	11.602388	0.000659	0.033592	0.067185	0.000237	0.000000	0.000426	0.000007
L6	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Porphyromonadaceae;g__Porphyromonas	12.715202	0.000363	0.040399	0.066736	0.000247	0.000000	0.001001	0.000036
L6	k__Bacteria;p__Firmicutes;Other;Other;Other	11.795661	0.000594	0.040399	0.109239	0.000316	0.000000	0.001087	0.000073
L6	k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Deinococcaceae;g__Deinococcus	11.602388	0.000659	0.040399	0.121196	0.000237	0.000000	0.000426	0.000007
L5	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae	9.803256	0.001742	0.046082	0.177687	0.000080	0.000000	0.000194	0.000007
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae	9.415884	0.002151	0.046082	0.219416	0.000163	0.000000	0.000718	0.000028
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae	8.931741	0.002803	0.046082	0.285862	0.001700	0.000262	0.005343	0.000604
L5	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;Other	8.907625	0.002840	0.046082	0.289662	0.000481	0.000076	0.002150	0.000153
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae	8.636156	0.003296	0.046082	0.336147	0.000941	0.000078	0.003787	0.000415
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;Other	8.468114	0.003614	0.046082	0.368654	0.000161	0.000000	0.000210	0.000015
L5	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae	8.205513	0.004176	0.047332	0.425986	0.001856	0.000079	0.005995	0.000472
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae	7.965916	0.004767	0.048620	0.486197	0.000158	0.000000	0.000438	0.000051
L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Ruminococcaceae;g__	10.148382	0.001444	0.053422	0.265747	0.008802	0.000551	0.010086	0.002110
L6	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Geodermatophilaceae;Other	9.803256	0.001742	0.053422	0.320534	0.000080	0.000000	0.000194	0.000007
L6	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Bifidobacteriales;f__Bifidobacteriaceae;Other	9.803256	0.001742	0.053422	0.320534	0.000081	0.000000	0.000920	0.000007
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae]	7.622365	0.005765	0.053456	0.588018	0.000078	0.000000	0.000939	0.000000
L5	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae	7.289453	0.006936	0.058956	0.707478	0.000627	0.000079	0.001570	0.000210
L6	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;Other;Other	8.907625	0.002840	0.065506	0.522528	0.000481	0.000076	0.002150	0.000153
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;f__Sphingomonadaceae;g__Kaistobacter	8.902307	0.002848	0.065506	0.524052	0.000079	0.000000	0.000163	0.000007
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;f__Rhodobacteraceae;g__Paracoccus	8.644261	0.003281	0.066296	0.603692	0.000163	0.000000	0.000456	0.000014
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;Other;Other	8.468114	0.003614	0.066296	0.665024	0.000161	0.000000	0.000210	0.000015
L6	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Comamonadaceae;Other	8.205513	0.004176	0.066296	0.768445	0.001856	0.000079	0.005995	0.000472
L6	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales;f__Oxalobacteraceae;g__Janthinobacterium	8.017965	0.004632	0.066296	0.852207	0.000627	0.000079	0.001347	0.000182
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Enhydrobacter	7.821488	0.005163	0.066296	0.949968	0.000244	0.000000	0.001868	0.000029
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales;f__Caulobacteraceae;Other	7.805989	0.005207	0.066296	0.958150	0.001623	0.000175	0.004623	0.000538
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae;g__Agrobacterium	7.681906	0.005578	0.066296	1.000000	0.000161	0.000000	0.000416	0.000044
L6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Alteromonadales;f__[Chromatiaceae];g__Rheinheimera	7.622365	0.005765	0.066296	1.000000	0.000078	0.000000	0.000203	0.000000
L6	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Moraxellaceae;g__Alkanindiges	7.425528	0.006430	0.069601	1.000000	0.000165	0.000000	0.000198	0.000021
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Aurantimonadaceae	6.559346	0.010433	0.080510	1.000000	0.000161	0.000000	0.000289	0.000029
L5	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae]	6.391304	0.011468	0.080510	1.000000	0.016227	0.002603	0.018571	0.006534
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Rhizobiaceae	6.334711	0.011840	0.080510	1.000000	0.000161	0.000000	0.000492	0.000117
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales;f__Pseudomonadaceae	6.098033	0.013533	0.082798	1.000000	0.000850	0.000079	0.001775	0.001669
L5	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Rikenellaceae	6.063600	0.013800	0.082798	1.000000	0.009502	0.004313	0.016193	0.004731
L4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales	5.829029	0.015764	0.085825	0.772427	0.000432	0.000000	0.001334	0.000072
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales;f__Xanthomonadaceae	5.829029	0.015764	0.089328	1.000000	0.000432	0.000000	0.001334	0.000072
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylocystaceae	5.600000	0.017960	0.096419	1.000000	0.000080	0.000000	0.000210	0.000059
L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__[Tissierellaceae];g__Peptoniphilus	6.731433	0.009473	0.096834	1.000000	0.003336	0.000535	0.004844	0.001375

M_MEAT_Diff-p-h

L	OTU	Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L5	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;Other	12.165692	0.000487	0.049650	0.049650	0.037587	0.005322	0.036616	0.007548
L5	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae]	9.987305	0.001576	0.053592	0.160776	0.000575	0.000000	0.000598	0.000028
L5	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae	9.987305	0.001576	0.053592	0.160776	0.000081	0.000000	0.000326	0.000009
L2	k__Bacteria;p__Deferribacteres	8.064422	0.004514	0.063200	0.063200	0.000080	0.000000	0.000682	0.000000
L5	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae	8.934902	0.002798	0.071342	0.285368	0.004134	0.000000	0.015916	0.000246
L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;Other;Other	12.165692	0.000487	0.072507	0.089565	0.037587	0.005322	0.036616	0.007548
L6	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfovibrionales;f__Desulfovibrionaceae;g__	10.009346	0.001557	0.072507	0.286576	0.000337	0.000000	0.000884	0.000000
L6	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__[Weeksellaceae];g__Cloacibacterium	9.987305	0.001576	0.072507	0.290026	0.000575	0.000000	0.000598	0.000028
L6	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Methylobacteriaceae;g__Methylobacterium	9.987305	0.001576	0.072507	0.290026	0.000081	0.000000	0.000326	0.000009
L3	k__Bacteria;p__Deferribacteres;c__Deferribacteres	8.064422	0.004514	0.078453	0.130914	0.000080	0.000000	0.000682	0.000000
L3	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae	7.736842	0.005411	0.078453	0.156905	0.005136	0.000237	0.006197	0.001781

L6	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Veillonellaceae;g__Veillonella	9.319171	0.002268	0.083451	0.417254	0.001125	0.000158	0.001890	0.000289
L5	k__Bacteria;p__Deferrribacteres;c__Deferrribacteres;o__Deferrribacterales;f__Deferrribacteraceae	8.064422	0.004514	0.083505	0.460457	0.000080	0.000000	0.000682	0.000000
L5	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales;f__Verrucomicrobiaceae	7.736842	0.005411	0.083505	0.551874	0.005136	0.000237	0.006197	0.001781
L5	k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales;f__Anaeroplasmataceae	7.633085	0.005731	0.083505	0.584534	0.000159	0.000000	0.000434	0.000018
L6	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales;f__Paenibacillaceae;g__Paenibacillus	8.934902	0.002798	0.085797	0.514781	0.004134	0.000000	0.015916	0.000246
L4	k__Bacteria;p__Deferrribacteres;c__Deferrribacteres;o__Deferrribacterales	8.064422	0.004514	0.093602	0.221200	0.000080	0.000000	0.000682	0.000000
L4	k__Bacteria;p__Verrucomicrobia;c__Verrucomicrobiae;o__Verrucomicrobiales	7.736842	0.005411	0.093602	0.265116	0.005136	0.000237	0.006197	0.001781
L4	k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales	7.633085	0.005731	0.093602	0.280805	0.000159	0.000000	0.000434	0.000018
L4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales	7.090719	0.007748	0.094918	0.379672	0.001069	0.000079	0.002057	0.000198
L5	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pasteurellales;f__Pasteurellaceae	7.090719	0.007748	0.098792	0.790338	0.001069	0.000079	0.002057	0.000198

M_POULT_Diff-p-h

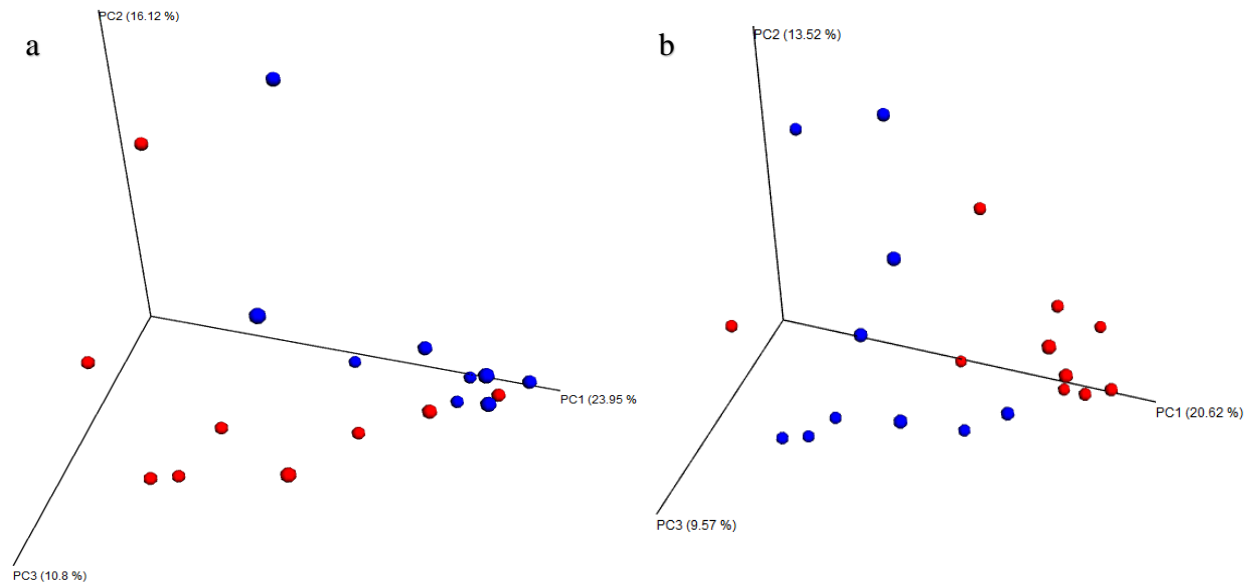
L	OTU	Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L3	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia	9.759230	0.001784	0.046358	0.051743	0.000000	0.000665	0.000222	0.000664
L3	k__Bacteria;p__Firmicutes;c__Clostridia	8.691429	0.003197	0.046358	0.092716	0.705732	0.434486	0.661241	0.433531
L4	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales	9.759230	0.001784	0.047523	0.087428	0.000000	0.000665	0.000222	0.000664
L4	k__Bacteria;p__Firmicutes;c__Bacilli;o__Bacillales	9.605714	0.001940	0.047523	0.095047	0.000710	0.009407	0.003821	0.045435
L4	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales	8.691429	0.003197	0.049882	0.156658	0.705732	0.434486	0.661241	0.433531
L4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales	8.251429	0.004072	0.049882	0.199528	0.000236	0.004081	0.001988	0.021900
L3	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria	7.260826	0.007047	0.068126	0.204377	0.000000	0.000553	0.000235	0.002407
L4	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales	7.260826	0.007047	0.069065	0.345327	0.000000	0.000553	0.000235	0.002407
L4	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Neisseriales	6.162162	0.013051	0.083703	0.639507	0.000000	0.000160	0.000016	0.000427
L4	k__Bacteria;p__Firmicutes;c__Erysipelotrichi;o__Erysipelotrichales	5.851429	0.015564	0.083703	0.762656	0.005183	0.040020	0.013116	0.042310
L4	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Xanthomonadales	5.575267	0.018216	0.083703	0.892578	0.000078	0.000364	0.001406	0.000778
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales	5.507994	0.018930	0.083703	0.927558	0.000198	0.001706	0.001215	0.004012
L4	k__Bacteria;p__Tenericutes;c__Mollicutes;o__Anaeroplasmatales	5.505268	0.018959	0.083703	0.929004	0.000000	0.000158	0.000049	0.000357
L4	k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Burkholderiales	5.491429	0.019110	0.083703	0.936386	0.003102	0.012797	0.009054	0.015575
L4	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales	5.368917	0.020499	0.083703	1.000000	0.000000	0.000359	0.000250	0.001849

M161_abs-B-h

L	OTU	Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L2	k__Bacteria;p__Bacteroidetes	7.426159	0.006428	0.089995	0.089995	0.116732	0.356100	0.143820	0.332204

VITD_SUPP_abs-B-h

L	OTU	Test-Statistic	P	FDR_P	Bonferroni_P	1_median	2_median	1_mean	2_mean
L2	k__Bacteria;Other	8.856382	0.002921	0.040889	0.040889	0.000161	0.000000	0.000312	0.000050
L3	k__Bacteria;Other;Other	8.856382	0.002921	0.084699	0.084699	0.000161	0.000000	0.000312	0.000050



Supplementary Figure. Bray-Curtis PCoA plots for a) percent-change in red meat consumption (PERMANOVA $p=0.026$) and b) percent-change in poultry consumption (PERMANOVA $p=0.011$). For both plots, red dots represent men in the lower half of the distribution of percent-change in consumption of the specific food group, while blue dots represent men in the upper half. From baseline to follow-up, changes in red meat consumption ranged from -1.9 to +2.8 ounces per day; changes in poultry consumption ranged from -3.9 to +5.8 ounces per day.